GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 18:39:08 ; Search time 266 Seconds
(without alignments)
268.908 Million cell updates/sec

Title: US-09-920-671-80
Perfect score: 20
Sequence: 1 caggtgtctcgatctccatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2356869 seqs, 1788235258 residues

Total number of hits satisfying chosen parameters: 1463878

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	11	US-09-920-671-80	Sequence 80, Appl
c 2	13.8	69.0	25	15	US-10-098-263B-59092	Sequence 59092, A
3	13.6	68.0	27	12	US-10-310-734-35	Sequence 35, Appl
4	13.6	68.0	27	13	US-10-123-101-35	Sequence 35, Appl
c 5	13.6	68.0	47	12	US-10-349-143-1075	Sequence 1075, Ap
6	13.6	68.0	47	12	US-10-349-143-1167	Sequence 1167, Ap
7	13.6	68.0	50	10	US-09-909-320-110	Sequence 110, App
8	13.6	68.0	50	10	US-09-909-088B-110	Sequence 110, App
9	13.6	68.0	50	10	US-09-905-291A-110	Sequence 110, App
10	13.6	68.0	50	10	US-09-902-853-110	Sequence 110, App
11	13.6	68.0	50	10	US-09-907-824-110	Sequence 110, App
12	13.6	68.0	50	10	US-09-907-841-110	Sequence 110, App
13	13.6	68.0	50	11	US-09-904-011-110	Sequence 110, App
14	13.6	68.0	50	11	US-09-906-742-110	Sequence 110, App
15	13.6	68.0	50	11	US-09-906-838-110	Sequence 110, App
16	13.6	68.0	50	11	US-09-907-613-110	Sequence 110, App
17	13.6	68.0	50	11	US-09-907-942-110	Sequence 110, App
18	13.6	68.0	50	11	US-09-904-859-110	Sequence 110, App
19	13.6	68.0	50	11	US-09-909-204-110	Sequence 110, App
20	13.6	68.0	50	11	US-09-904-820-110	Sequence 110, App
21	13.6	68.0	50	11	US-09-904-786-110	Sequence 110, App
22	13.6	68.0	50	11	US-09-906-646-110	Sequence 110, App
23	13.6	68.0	50	11	US-09-906-700-110	Sequence 110, App
24	13.6	68.0	50	11	US-09-903-786-110	Sequence 110, App
25	13.6	68.0	50	11	US-09-902-903-110	Sequence 110, App
26	13.6	68.0	50	11	US-09-903-749A-110	Sequence 110, App
27	13.6	68.0	50	11	US-09-904-119-110	Sequence 110, App
28	13.6	68.0	50	11	US-09-904-956-110	Sequence 110, App
29	13.6	68.0	50	11	US-09-902-736-110	Sequence 110, App
30	13.6	68.0	50	11	US-09-907-794-110	Sequence 110, App
31	13.6	68.0	50	11	US-09-903-943-110	Sequence 110, App
32	13.6	68.0	50	11	US-09-904-462-110	Sequence 110, App
33	13.6	68.0	50	11	US-09-907-925-110	Sequence 110, App
34	13.6	68.0	50	11	US-09-902-692-110	Sequence 110, App
35	13.6	68.0	50	11	US-09-903-520-110	Sequence 110, App
36	13.6	68.0	50	11	US-09-905-056-110	Sequence 110, App
37	13.6	68.0	50	11	US-09-909-064-110	Sequence 110, App
38	13.6	68.0	50	11	US-09-904-553-110	Sequence 110, App
39	13.6	68.0	50	11	US-09-905-381-110	Sequence 110, App
40	13.6	68.0	50	11	US-09-905-088-110	Sequence 110, App
41	13.6	68.0	50	11	US-09-907-575-110	Sequence 110, App
42	13.6	68.0	50	11	US-09-905-075-110	Sequence 110, App
43	13.6	68.0	50	11	US-09-902-759-110	Sequence 110, App
44	13.6	68.0	50	11	US-09-902-634-110	Sequence 110, App
45	13.6	68.0	50	11	US-09-902-713-110	Sequence 110, App

ALIGNMENTS

RESULT 1
US-09-920-671-80
; Sequence 80, Application US/09920671
; Publication No. US20030083283A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF COREST EXPRESSION
; FILE REFERENCE: RTS-0297
; CURRENT APPLICATION NUMBER: US/09/920,671
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 80
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-671-80

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
||||||||||||||||||||
Db 1 CAGGTGTCTCGATCTCCATG 20

RESULT 2
US-10-098-263B-59092/c
; Sequence 59092, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B

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;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 59092
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-59092

  Query Match             69.0%;  Score 13.8;  DB 15;  Length 25;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGTGTCTCGATCTCCAT 19
              ||||||| | |||||||
Db         21 GGTGTCTTGTTCTCCAT 5


RESULT 3
US-10-310-734-35
; Sequence 35, Application US/10310734
; Publication No. US20030232324A1
; GENERAL INFORMATION:
;  APPLICANT: POLO, John
;  APPLICANT:  PERRI, Silvia
;  APPLICANT:  THUDIUM, Kent
;  APPLICANT:  TANG, Zequn
;  TITLE OF INVENTION: CHIMERIC ALPHAVIRUS REPLICON PARTICLES
;  FILE REFERENCE: CHIR-17924/02US (2300-17924.20)
;  CURRENT APPLICATION NUMBER: US/10/310,734
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: 10/123,101
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 125
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: VE2F
US-10-310-734-35

  Query Match             68.0%;  Score 13.6;  DB 12;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              |||| | ||| ||| |||||
Db          7 CAGGGGACTCCATCACCATG 26


RESULT 4
US-10-123-101-35
; Sequence 35, Application US/10123101
; Publication No. US20030148262A1
; GENERAL INFORMATION:
;  APPLICANT: POLO, John
;  APPLICANT:  PERRI, Silvia
;  APPLICANT:  THUDIUM, Kent
;  TITLE OF INVENTION: CHIMERIC ALPHAVIRUS REPLICON PARTICLES
;  FILE REFERENCE: 2300-17924 / PP17924.002
;  CURRENT APPLICATION NUMBER: US/10/123,101
;  CURRENT FILING DATE:  2002-07-23
;  PRIOR APPLICATION NUMBER: 60/295,451
;  PRIOR FILING DATE: 2001-05-31
;  NUMBER OF SEQ ID NOS: 92
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: VE2F
US-10-123-101-35

  Query Match             68.0%;  Score 13.6;  DB 13;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              |||| | ||| ||| |||||
Db          7 CAGGGGACTCCATCACCATG 26


RESULT 5
US-10-349-143-1075/c
; Sequence 1075, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1075
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: 99-2027-296 : polymorphic base A or G
US-10-349-143-1075

  Query Match             68.0%;  Score 13.6;  DB 12;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              ||| ||| || |||| ||||
Db         46 CAGATGTATCCATCTGCATG 27


RESULT 6
US-10-349-143-1167
; Sequence 1167, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1167
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2085-172 : polymorphic base C or T
US-10-349-143-1167

Query Match 68.0%; Score 13.6; DB 12; Length 47;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
||| ||| || |||| ||||
Db 2 CAGATGTATCCATCTGCATG 21

RESULT 7
US-09-909-320-110
; Sequence 110, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-909-320-110

Query Match 68.0%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|| |||||||||| | |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 8
US-09-909-088B-110
; Sequence 110, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22

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;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide probe
US-09-909-088B-110

  Query Match             68.0%;  Score 13.6;  DB 10;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| | |||
Db         24 CAAGTGTCTCGATGTGGATG 43


RESULT 9
US-09-905-291A-110
; Sequence 110, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,291A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide probe
US-09-905-291A-110

  Query Match             68.0%;  Score 13.6;  DB 10;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| | |||
Db         24 CAAGTGTCTCGATGTGGATG 43


RESULT 10
US-09-902-853-110
; Sequence 110, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
```

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-902-853-110

Query Match 68.0%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| |  |||
Db         24 CAAGTGTCTCGATGTGGATG 43
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RESULT 11
US-09-907-824-110
; Sequence 110, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-824-110

Query Match 68.0%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|| |||||||||| | |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 12
US-09-907-841-110
; Sequence 110, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-907-841-110

Query Match 68.0%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|| |||||||||| | |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 13
US-09-904-011-110
; Sequence 110, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-011-110

  Query Match   68.0%; Score 13.6; DB 11; Length 50;
  Best Local Similarity   80.0%; Pred. No. 3.3e+03;
  Matches   16; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| | |||
Db   24 CAAGTGTCTCGATGTGGATG 43

RESULT 14
US-09-906-742-110
; Sequence 110, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-906-742-110

  Query Match   68.0%; Score 13.6; DB 11; Length 50;
  Best Local Similarity   80.0%; Pred. No. 3.3e+03;
  Matches   16; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| | |||
Db   24 CAAGTGTCTCGATGTGGATG 43

RESULT 15
US-09-906-838-110
; Sequence 110, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

```
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,838
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-906-838-110

  Query Match            68.0%;  Score 13.6;  DB 11;  Length 50;
  Best Local Similarity  80.0%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| |  |||
Db         24 CAAGTGTCTCGATGTGGATG 43
```

Search completed: January 28, 2004, 19:46:33
Job time : 270 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 18:37:22 ; Search time 76 Seconds
(without alignments)
116.153 Million cell updates/sec

Title: US-09-920-671-80
Perfect score: 20
Sequence: 1 caggtgtctcgatctccatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 809828

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13.8	69.0	21	4	US-09-099-053-24	Sequence 24, Appl
c 2	13.6	68.0	30	4	US-09-638-649-9	Sequence 9, Appli
c 3	13.6	68.0	47	4	US-09-422-978-1075	Sequence 1075, Ap
4	13.6	68.0	47	4	US-09-422-978-1167	Sequence 1167, Ap
5	13.6	68.0	61	3	US-09-023-228B-41	Sequence 41, Appl
6	13.6	68.0	61	4	US-09-163-025B-41	Sequence 41, Appl
7	13.6	68.0	61	4	US-10-037-282-41	Sequence 41, Appl
c 8	13.2	66.0	39	1	US-08-431-896B-5	Sequence 5, Appli
9	13.2	66.0	60	3	US-09-023-228B-36	Sequence 36, Appl
10	13.2	66.0	60	4	US-09-163-025B-36	Sequence 36, Appl
11	13.2	66.0	60	4	US-10-037-282-36	Sequence 36, Appl
12	13.2	66.0	64	1	US-08-431-896B-7	Sequence 7, Appli
c 13	13.2	66.0	66	1	US-08-431-896B-4	Sequence 4, Appli
14	13	65.0	66	4	US-09-209-525-19	Sequence 19, Appl
15	12.8	64.0	20	3	US-09-311-260-98	Sequence 98, Appl
16	12.8	64.0	47	4	US-09-422-978-2736	Sequence 2736, Ap
c 17	12.8	64.0	47	4	US-09-422-978-2965	Sequence 2965, Ap
18	12.6	63.0	20	4	US-09-183-636-3	Sequence 3, Appli
19	12.6	63.0	21	2	US-08-117-952-688	Sequence 688, App
20	12.6	63.0	26	1	US-08-261-206A-67	Sequence 67, Appl
c 21	12.6	63.0	27	3	US-08-776-971-83	Sequence 83, Appl
22	12.6	63.0	42	2	US-08-379-057-54	Sequence 54, Appl
c 23	12.6	63.0	63	1	US-08-198-431-38	Sequence 38, Appl
c 24	12.6	63.0	63	1	US-08-564-955-38	Sequence 38, Appl
c 25	12.6	63.0	63	2	US-08-537-874-38	Sequence 38, Appl
c 26	12.6	63.0	63	3	US-08-621-859-38	Sequence 38, Appl
c 27	12.6	63.0	63	3	US-09-100-856A-38	Sequence 38, Appl
c 28	12.6	63.0	63	3	US-09-075-511-38	Sequence 38, Appl
c 29	12.6	63.0	63	3	US-09-099-015-38	Sequence 38, Appl
c 30	12.6	63.0	63	3	US-09-232-863-38	Sequence 38, Appl
c 31	12.6	63.0	63	3	US-09-133-508A-38	Sequence 38, Appl
c 32	12.6	63.0	63	3	US-09-165-060-38	Sequence 38, Appl
c 33	12.6	63.0	63	3	US-09-501-698-38	Sequence 38, Appl
c 34	12.6	63.0	63	4	US-09-240-310-38	Sequence 38, Appl
c 35	12.6	63.0	63	4	US-09-590-778-38	Sequence 38, Appl
c 36	12.6	63.0	63	4	US-09-477-763-38	Sequence 38, Appl
c 37	12.6	63.0	63	4	US-09-590-774-38	Sequence 38, Appl
c 38	12.6	63.0	63	4	US-09-619-550-38	Sequence 38, Appl
c 39	12.6	63.0	63	4	US-09-240-734-38	Sequence 38, Appl
c 40	12.6	63.0	63	4	US-09-231-253-38	Sequence 38, Appl
c 41	12.6	63.0	63	4	US-09-724-958-38	Sequence 38, Appl
c 42	12.6	63.0	63	4	US-09-696-322-38	Sequence 38, Appl
c 43	12.6	63.0	63	4	US-09-717-391-38	Sequence 38, Appl
c 44	12.6	63.0	63	4	US-09-696-313-38	Sequence 38, Appl
c 45	12.6	63.0	63	4	US-09-240-307-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-099-053-24/c
; Sequence 24, Application US/09099053
; Patent No. 6388063
; GENERAL INFORMATION:
; APPLICANT: Greg Plowman
; APPLICANT: Susan Onrust
; APPLICANT: David Markby
; APPLICANT: Sara Courtneidge
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SAD RELATED DISORDERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,053
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/049,914
; FILING DATE: June 18, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 235/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-099-053-24

Query Match 69.0%; Score 13.8; DB 4; Length 21;

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  Best Local Similarity   88.2%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GTGTCTCGATCTCCATG 20
              |||||| ||||||| ||
Db         21 GTGTCTGGATCTCCTTG 5


RESULT 2
US-09-638-649-9/c
; Sequence 9, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
;  APPLICANT:  Stern, David M.
;  APPLICANT:  Schmidt, Ann Marie
;  APPLICANT:  Yan, Shi Du
;  TITLE OF INVENTION:  TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
;  TITLE OF INVENTION:  GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  0575/62175
;  CURRENT APPLICATION NUMBER: US/09/638,649
;  CURRENT FILING DATE:  2000-08-14
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  PCR Primers
US-09-638-649-9

  Query Match             68.0%;  Score 13.6;  DB 4;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              |||||||||||||  | | ||
Db         22 CAGGTGTCTCGAGATACTTG 3


RESULT 3
US-09-422-978-1075/c
; Sequence 1075, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1075
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: 99-2027-296 : polymorphic base A or G
US-09-422-978-1075

  Query Match             68.0%;  Score 13.6;  DB 4;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              ||| ||| || |||| ||||
Db         46 CAGATGTATCCATCTGCATG 27


RESULT 4
US-09-422-978-1167
; Sequence 1167, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1167
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: 99-2085-172 : polymorphic base C or T
US-09-422-978-1167

  Query Match             68.0%;  Score 13.6;  DB 4;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              ||| ||| || |||| ||||
Db          2 CAGATGTATCCATCTGCATG 21


RESULT 5
US-09-023-228B-41
; Sequence 41, Application US/09023228B
; Patent No. 6140490
;  GENERAL INFORMATION:
;    APPLICANT:  BIESECKER, GREGORY
;    APPLICANT:  GOLD, LARRY
;    TITLE OF INVENTION:  HIGH AFFINITY NUCLEIC ACID LIGANDS OF
;    TITLE OF INVENTION:  COMPLEMENT SYSTEM PROTEINS
;    NUMBER OF SEQUENCES:  157
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Place #200
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  US
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,228B
;      FILING DATE:  12-FEBRUARY-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US97/01739
;      FILING DATE:  30 JAN 1997
;    PRIOR APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  08/595,335
;       FILING DATE:  1 FEB 1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Barry J. Swanson, Esq.
;       REGISTRATION NUMBER:  33,215
;       REFERENCE/DOCKET NUMBER:  NEX50/CIP
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 793-3333
;       TELEFAX:  (303) 793-3433
;   INFORMATION FOR SEQ ID NO:  41:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  61 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  RNA
;     FEATURE:
;       OTHER INFORMATION:  All pyrimidines are 2'-F modified
US-09-023-228B-41

  Query Match             68.0%;  Score 13.6;  DB 3;  Length 61;
  Best Local Similarity   60.0%;  Pred. No. 4.8e+02;
  Matches   12;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              | || |:|:||| |:| |:|
Db         13 CGGGCGUCUCGAGCUCUAUG 32


RESULT 6
US-09-163-025B-41
; Sequence 41, Application US/09163025B
; Patent No. 6395888
; GENERAL INFORMATION:
;  APPLICANT: NeXstar Pharmaceuticals, Inc.
;  TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF COMPLEMENT SYSTEM
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: NEX 50 CIP2
;  CURRENT APPLICATION NUMBER: US/09/163,025B
;  CURRENT FILING DATE:  1998-09-29
;  PRIOR APPLICATION NUMBER: 09/023,228
;  PRIOR FILING DATE: 1998-02-12
;  PRIOR APPLICATION NUMBER: PCT/US97/01739
;  PRIOR FILING DATE: 1997-01-30
;  NUMBER OF SEQ ID NOS: 198
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 61
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Completely
;   OTHER INFORMATION: Synthesized Nucleic Acid
;   NAME/KEY: modified_base
;   LOCATION: (1)..(61)
;   OTHER INFORMATION: All c's and u's are 2'-F
US-09-163-025B-41

  Query Match             68.0%;  Score 13.6;  DB 4;  Length 61;
  Best Local Similarity   60.0%;  Pred. No. 4.8e+02;
  Matches   12;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              | || |:|:||| |:| |:|
Db         13 CGGGCGUCUCGAGCUCUAUG 32


RESULT 7
US-10-037-282-41
; Sequence 41, Application US/10037282
; Patent No. 6566343
; GENERAL INFORMATION:
;  APPLICANT: BIESECKER, GREGORY
;  APPLICANT:  GOLD, LARRY
;  TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF COMPLEMENT SYSTEM
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: NEX 50 CIP 2 CON
;  CURRENT APPLICATION NUMBER: US/10/037,282
;  CURRENT FILING DATE:  2002-01-03
;  PRIOR APPLICATION NUMBER: 09/163,025
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: 08/595,335
;  PRIOR FILING DATE: 1996-02-01
;  PRIOR APPLICATION NUMBER: PCT/US97/01739
;  PRIOR FILING DATE: 1997-01-30
;  NUMBER OF SEQ ID NOS: 198
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 61
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
;   OTHER INFORMATION: all pyrimidines are 2'F
US-10-037-282-41

  Query Match             68.0%;  Score 13.6;  DB 4;  Length 61;
  Best Local Similarity   60.0%;  Pred. No. 4.8e+02;
  Matches   12;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              | || |:|:||| |:| |:|
Db         13 CGGGCGUCUCGAGCUCUAUG 32


RESULT 8
US-08-431-896B-5/c
; Sequence 5, Application US/08431896B
; Patent No. 5773244
;  GENERAL INFORMATION:
;    APPLICANT:  Ares, Manuel, Jr.
;    APPLICANT:  Ford, Ethan E.
;    TITLE OF INVENTION:  RNA Cyclase Ribozymes
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,896B
;      FILING DATE:  01-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/063,857
;      FILING DATE:  19-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Kenneth A.
;      REGISTRATION NUMBER:  31,677
;      REFERENCE/DOCKET NUMBER:  02307E-070000US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
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;    MOLECULE TYPE:  RNA
US-08-431-896B-5

  Query Match             66.0%;  Score 13.2;  DB 1;  Length 39;
  Best Local Similarity   83.3%;  Pred. No. 7.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGTGTCTCGATCTCCATG 20
              |||  ||||| |||||||
Db         22 GGTACCTCGAGCTCCATG 5


RESULT 9
US-09-023-228B-36
; Sequence 36, Application US/09023228B
; Patent No. 6140490
;  GENERAL INFORMATION:
;    APPLICANT:  BIESECKER, GREGORY
;    APPLICANT:  GOLD, LARRY
;    TITLE OF INVENTION:  HIGH AFFINITY NUCLEIC ACID LIGANDS OF
;    TITLE OF INVENTION:  COMPLEMENT SYSTEM PROTEINS
;    NUMBER OF SEQUENCES:  157
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Place #200
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  US
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,228B
;      FILING DATE:  12-FEBRUARY-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US97/01739
;      FILING DATE:  30 JAN 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/595,335
;      FILING DATE:  1 FEB 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson, Esq.
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX50/CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  60 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
;    FEATURE:
;      OTHER INFORMATION:  All pyrimidines are 2'-F modified
US-09-023-228B-36

  Query Match             66.0%;  Score 13.2;  DB 3;  Length 60;
  Best Local Similarity   61.1%;  Pred. No. 7.6e+02;
  Matches   11;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGTGTCTCGATCTCCATG 20
              || |:|:||| |:| |:|
Db         14 GGCGUCUCGAGCUCUAUG 31


RESULT 10
US-09-163-025B-36
; Sequence 36, Application US/09163025B
; Patent No. 6395888
; GENERAL INFORMATION:
;  APPLICANT: NeXstar Pharmaceuticals, Inc.
;  TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF COMPLEMENT SYSTEM
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: NEX 50 CIP2
;  CURRENT APPLICATION NUMBER: US/09/163,025B
;  CURRENT FILING DATE:  1998-09-29
;  PRIOR APPLICATION NUMBER: 09/023,228
;  PRIOR FILING DATE: 1998-02-12
;  PRIOR APPLICATION NUMBER: PCT/US97/01739
;  PRIOR FILING DATE: 1997-01-30
;  NUMBER OF SEQ ID NOS: 198
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 60
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Completely
;   OTHER INFORMATION: Synthesized Nucleic Acid
;   NAME/KEY: modified_base
;   LOCATION: (1)..(60)
;   OTHER INFORMATION: All c's and u's are 2'-F
US-09-163-025B-36

  Query Match             66.0%;  Score 13.2;  DB 4;  Length 60;
  Best Local Similarity   61.1%;  Pred. No. 7.6e+02;
  Matches   11;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGTGTCTCGATCTCCATG 20
              || |:|:||| |:| |:|
Db         14 GGCGUCUCGAGCUCUAUG 31


RESULT 11
US-10-037-282-36
; Sequence 36, Application US/10037282
; Patent No. 6566343
; GENERAL INFORMATION:
;  APPLICANT: BIESECKER, GREGORY
;  APPLICANT:  GOLD, LARRY
;  TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF COMPLEMENT SYSTEM
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: NEX 50 CIP 2 CON
;  CURRENT APPLICATION NUMBER: US/10/037,282
;  CURRENT FILING DATE:  2002-01-03
;  PRIOR APPLICATION NUMBER: 09/163,025
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: 08/595,335
;  PRIOR FILING DATE: 1996-02-01
;  PRIOR APPLICATION NUMBER: PCT/US97/01739
;  PRIOR FILING DATE: 1997-01-30
;  NUMBER OF SEQ ID NOS: 198
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 60
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
;   OTHER INFORMATION: all pyrimidines are 2'F
US-10-037-282-36

  Query Match             66.0%;  Score 13.2;  DB 4;  Length 60;
  Best Local Similarity   61.1%;  Pred. No. 7.6e+02;
  Matches   11;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGTGTCTCGATCTCCATG 20
              || |:|:||| |:| |:|
Db         14 GGCGUCUCGAGCUCUAUG 31
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RESULT 12
US-08-431-896B-7
; Sequence 7, Application US/08431896B
; Patent No. 5773244
;  GENERAL INFORMATION:
;    APPLICANT:  Ares, Manuel, Jr.
;    APPLICANT:  Ford, Ethan E.
;    TITLE OF INVENTION:  RNA Cyclase Ribozymes
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,896B
;      FILING DATE:  01-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/063,857
;      FILING DATE:  19-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Kenneth A.
;      REGISTRATION NUMBER:  31,677
;      REFERENCE/DOCKET NUMBER:  02307E-070000US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  64 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-431-896B-7

  Query Match             66.0%;  Score 13.2;  DB 1;  Length 64;
  Best Local Similarity   83.3%;  Pred. No. 7.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGTGTCTCGATCTCCATG 20
              |||  |||||  |||||||
Db         33 GGTACCTCGAGCTCCATG 50


RESULT 13
US-08-431-896B-4/c
; Sequence 4, Application US/08431896B
; Patent No. 5773244
;  GENERAL INFORMATION:
;    APPLICANT:  Ares, Manuel, Jr.
;    APPLICANT:  Ford, Ethan E.
;    TITLE OF INVENTION:  RNA Cyclase Ribozymes
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,896B
;      FILING DATE:  01-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/063,857
;      FILING DATE:  19-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Kenneth A.
;      REGISTRATION NUMBER:  31,677
;      REFERENCE/DOCKET NUMBER:  02307E-070000US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  66 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-431-896B-4

  Query Match             66.0%;  Score 13.2;  DB 1;  Length 66;
  Best Local Similarity   83.3%;  Pred. No. 7.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGTGTCTCGATCTCCATG 20
              |||  |||||  |||||||
Db         29 GGTACCTCGAGCTCCATG 12


RESULT 14
US-09-209-525-19
; Sequence 19, Application US/09209525
; Patent No. 6303770
; GENERAL INFORMATION:
;  APPLICANT: Lok, Si
;  APPLICANT: Conklin, Darrell C.
;  APPLICANT: Parrish, Julia E.
;  TITLE OF INVENTION: Mammalian Alpha Helical Protein-1
;  FILE REFERENCE: 97-71
;  CURRENT APPLICATION NUMBER: US/09/209,525
;  CURRENT FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 66
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-209-525-19

  Query Match             65.0%;  Score 13;  DB 4;  Length 66;
  Best Local Similarity   100.0%;  Pred. No. 9.6e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TCTCGATCTCCAT 19
              |||||||||||||
Db         33 TCTCGATCTCCAT 45


RESULT 15
US-09-311-260-98
; Sequence 98, Application US/09311260
; Patent No. 6214555
;  GENERAL INFORMATION:
;    APPLICANT:  Leushner, James
;    APPLICANT:  Hui, May
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  LaCroix, Jean-Michel
;    TITLE OF INVENTION:  METHOD, COMPOSITIONS AND KIT FOR DETECTION OF
;    TITLE OF INVENTION:  MICROORGANISMS AND BI-DIRECTIONAL SEQUENCING OF NUCLEIC ACID
```

; TITLE OF INVENTION: POLYMERS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson LLP
; STREET: P.O. Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: US
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-058-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2082
; TELEX:
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
US-09-311-260-98

Query Match 64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          5 TGTCTCGATCTCCATG 20
              | ||| ||||||||||
Db          5 TTTCTTGATCTCCATG 20
```

Search completed: January 28, 2004, 18:43:31
Job time : 92 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 18:36:28 ; Search time 153 Seconds
(without alignments)
352.868 Million cell updates/sec

Title: US-09-920-671-80
Perfect score: 20
Sequence: 1 caggtgtctcgatctccatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2667462

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
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8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
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19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	13.8	69.0	21	20	AAV81773	Human SAD PCR prim
c	2	13.8	69.0	41	19	AAV18872	Primer for rat hyp
c	3	13.8	69.0	63	21	AAC10340	Human secreted pro
	4	13.6	68.0	27	25	ABZ23027	VEE and SIN replic
c	5	13.6	68.0	47	21	AAZ66728	Human map-related
	6	13.6	68.0	47	21	AAZ66820	Human map-related
	7	13.6	68.0	50	20	AAX52340	Primer 28744.p (OL
	8	13.6	68.0	50	20	AAX28444	EGF-like/FGF-8 hom
	9	13.6	68.0	50	21	AAA77544	Human PRO214 hybri
	10	13.6	68.0	50	21	AAA30035	Probe used in PRO2
	11	13.6	68.0	50	22	AAF60355	PRO214 probe #1.
	12	13.6	68.0	50	22	AAF72498	Human PRO polypept
	13	13.6	68.0	50	23	ABL01039	Human SNP involvin
	14	13.6	68.0	50	24	ABK40295	Oligonucleotide pr
	15	13.6	68.0	50	25	ACA54898	Secreted and trans
	16	13.6	68.0	50	25	ACA58383	Probe #21 used to
	17	13.6	68.0	50	25	ACA60090	Human secreted/tra
	18	13.6	68.0	50	25	ACA05428	Human secreted pro
	19	13.6	68.0	50	25	ABX96107	Human secreted/tra
	20	13.6	68.0	50	25	ABX71538	Human secreted/tra
	21	13.6	68.0	61	20	AAZ19588	Complement system
c	22	13.6	68.0	65	24	ABN31465	Rat spliced transc
c	23	13.6	68.0	65	24	ABN51168	Mouse spliced tran
c	24	13.4	67.0	21	21	AAZ36007	Forward PCR primer
	25	13.4	67.0	26	24	ABZ29883	Candida albicans G
c	26	13.4	67.0	33	24	ABA04774	F-cassette structu
c	27	13.4	67.0	41	24	ABA04776	F-cassette structu
	28	13.4	67.0	50	24	ABZ01618	Human leukocyte ge
c	29	13.4	67.0	51	22	AAI78748	Human silent SNP c
c	30	13.2	66.0	50	24	ABZ04252	Human leukocyte ge
c	31	13.2	66.0	50	24	AAL50075	Mammalian sialyltr
	32	13.2	66.0	51	22	AAL27124	Human SNP oligonuc
	33	13.2	66.0	57	22	AAF54785	PCR primer used to
	34	13.2	66.0	60	20	AAZ19583	Complement system
	35	13.2	66.0	65	24	ABN53230	Mouse spliced tran
c	36	13.2	66.0	75	22	AAC91193	Portion of Ad5 DNA
	37	13	65.0	66	20	AAX80701	Human Zalpha1 cDNA
	38	13	65.0	66	24	ABN83098	Human alpha helica
	39	13	65.0	66	24	ABK12068	Antisense oligo ZC
	40	12.8	64.0	19	22	AAI66133	Human glaucoma-cod
	41	12.8	64.0	20	22	AAH03074	Microorganism dete
c	42	12.8	64.0	40	23	ABK85851	Caspase-3 large su
c	43	12.8	64.0	40	23	ABK49941	HMFG1/Caspase-3 fu
c	44	12.8	64.0	40	23	ABK50184	HMFG1 Fab/Caspase-
c	45	12.8	64.0	47	21	AAZ68616	Human map-related

ALIGNMENTS

RESULT 1
AAV81773/c
ID AAV81773 standard; DNA; 21 BP.
XX
AC AAV81773;
XX
DT 10-MAR-1999 (first entry)
XX
DE Human SAD PCR primer 5284.
XX
KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9849317-A2.
XX
PD 05-NOV-1998.
XX
PF 27-APR-1998; 98WO-US08439.
XX
PR 23-OCT-1997; 97US-0063595.
PR 28-APR-1997; 97US-0044428.
PR 20-MAY-1997; 97US-0047222.
PR 11-JUN-1997; 97US-0049477.
PR 11-JUN-1997; 97US-0049756.
PR 18-JUN-1997; 97US-0049914.
XX

PA (SUGE-) SUGEN INC.
XX
PI App H, Clary D, Courtneidge SA, Hui TH, Jallal B;
PI Markby D, Onrust S, Peles E, Plowman GD;
XX
DR WPI; 1999-009434/01.
XX
PT New nucleic acid encoding specific protein tyrosine phosphatases -
PT useful for identifying specific modulators for treatment and
PT prevention of cancer and neurodegenerative disease
XX
PS Example 7; Page 90; 193pp; English.
XX
CC The present invention describes isolated, enriched or purified nucleic
CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
CC above proteins, other than ALK-7, are protein tyrosine phosphatases
CC (PTPs) and are used to identify substances that modulate their activity
CC (i.e. agonists and antagonists, including NBP) in vivo or in vitro.
CC These substances are used to treat or prevent diseases associated with
CC abnormal signal transduction pathways that involve the proteins,
CC particularly cancer (e.g. leukaemia and lymphoma), while modulators of
CC ALK-7 (which is a type I receptor serine/threonine kinase) are used to
CC promote neuronal survival, particularly for treating Alzheimer's,
CC Parkinson's or Huntington's diseases. Nucleic acid fragments of the
CC polynucleotides encoding the proteins can be used as probes to identify
CC and clone related sequences; to detect protein-encoded RNA; to generate
CC transgenic animals and in gene therapy (optionally after mutation). Ab
CC are used to determine the proteins. The present sequence represents a
CC PCR primer for human SAD.
XX
SQ Sequence 21 BP; 7 A; 7 C; 5 G; 2 T; 0 other;

Query Match 69.0%; Score 13.8; DB 20; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTGTCTCGATCTCCATG 20
||||||| ||||||| ||
Db 21 GTGTCTGGATCTCCTTG 5

RESULT 2
AAV18872/c
ID AAV18872 standard; DNA; 41 BP.
XX
AC AAV18872;
XX
DT 09-JUL-1998 (first entry)
XX
DE Primer for rat hypocretin 35 cDNA.
XX
KW Rat; hypocretin 35; H35; treatment; neurological disease;
KW homeostatic dysfunction; PCR primer;
KW homeostatic regulatory hormone production; ss.
XX
OS Synthetic.
OS Rattus rattus.
XX
PN WO9805352-A1.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-US13657.
XX
PR 02-AUG-1996; 96US-0023220.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Bloom FE, Danielson PE, De Lecea L, Foye PE, Gautvik KM;
PI Gautvik VT, Kilduff TS, Sutcliffe JG;
XX
DR WPI; 1998-145352/13.
XX
PT Nucleic acid encoding hypocretin of rat and mouse - useful for
PT diagnosis and treatment of neurological disease, homeostatic
PT dysfunction etc., also sequence for calmodulin kinase-like protein
XX
PS Example 3; Page 73; 111pp; English.
XX
CC The present sequence is a primer for the cDNA encoding rat
CC hypocretin 35 (H35), which is involved in lowering body temperature
CC and reducing food intake.
CC Modulation of the H35 receptor can be used in the treatment of
CC neurological disease or homeostatic dysfunction, or to control
CC homeostatic regulatory hormone production. Hypocretin proteins can
CC be used to raise antibodies (Ab), to identify specific agonists or
CC antagonists, in therapy, to detect Ab and to isolate cognate
CC receptors. Oligonucleotides based on H35 cDNA can be used to detect
CC the hypocretin gene or its RNA transcript, and as antisense agents
CC for inhibiting gene expression. H35 cDNA can also be used for
CC recombinant protein production. The Ab can be used to detect or
CC quantify hypocretin proteins and as a therapeutic inhibitor.
XX
SQ Sequence 41 BP; 13 A; 11 C; 6 G; 11 T; 0 other;

Query Match 69.0%; Score 13.8; DB 19; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTGTCTCGATCTCCAT 19
||||||| |||||| ||
Db 17 GGTGTCTAGATCTCGAT 1

RESULT 3
AAC10340/c
ID AAC10340 standard; cDNA; 63 BP.
XX
AC AAC10340;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 14415.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 14415; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences

CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 63 BP; 14 A; 14 C; 25 G; 9 T; 1 other;

Query Match 69.0%; Score 13.8; DB 21; Length 63;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTGTCTCGATCTCCAT 19
||||||| | |||||||
Db 57 GGTGTCTGGGTCTCCAT 41

RESULT 4
ABZ23027
ID ABZ23027 standard; DNA; 27 BP.
XX
AC ABZ23027;
XX
DT 11-APR-2003 (first entry)
XX
DE VEE and SIN replicon particle chimera related PCR primer SEQ ID NO:35.
XX
KW Chimeric alphavirus; alphavirus replicon particle; vaccine; gene therapy;
KW immune response; gene delivery; structural protein; Sindbis virus; SIN;
KW VEE; venezuelan equine encephalitis virus; PCR primer; ss.
XX
OS Sindbis virus.
OS Venezuelan equine encephalitis virus.
OS Synthetic.
XX
PN WO200299035-A2.
XX
PD 12-DEC-2002.
XX
PF 11-APR-2002; 2002WO-US11585.
XX
PR 31-MAY-2001; 2001US-295451P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Polo J, Perri S, Thudium K;
XX
DR WPI; 2003-140604/13.
XX
PT Novel chimeric alphavirus particle, useful for generating an immune
PT response in a mammal, has RNA derived from one or more alphaviruses,
PT and structural proteins derived from two or more alphaviruses -
XX
PS Example 4; Page 66; 104pp; English.
XX
CC The present invention describes a chimeric alphavirus particle (I),
CC comprising RNA derived from one or more alphaviruses, and structural
CC proteins derived from two or more alphaviruses. Also described is an
CC alphavirus replicon RNA (II) comprising a 5' sequence required for
CC nonstructural protein-mediated amplification, sequences encoding
CC biologically active alphavirus nonstructural proteins, an alphavirus
CC subgenomic promoter, a non-alphavirus heterologous sequence, and a 3'
CC sequence required for nonstructural protein-mediated amplification, where
CC the sequence encoding at least one of the nonstructural proteins is
CC derived from a Biosafety Level 3 (BSL-3) alphavirus and where the
CC sequences of the replicon RNA exhibit sequence identity to at least one
CC third but no more than two-thirds of a genome of a BSL-3 alphavirus. (I)
CC can be used in vaccines and in gene therapy. (I) is useful for generating
CC an immune response in a mammal, by administering (I) to the mammal so
CC generating an immune response. (I) and (II) are useful as gene delivery
CC vehicles having altered cell and tissue tropism, and/or structural
CC protein surface antigenicity. (I) is also useful in the ex vivo and
CC in vivo administration of heterologous genes having therapeutic or
CC prophylactic applications. The present sequence represents a PCR primer
CC which is used in an example from the present invention for the generation
CC of alphavirus replicon particle chimeras with hybrid glycoproteins.
XX
SQ Sequence 27 BP; 8 A; 7 C; 6 G; 6 T; 0 other;

Query Match 68.0%; Score 13.6; DB 25; Length 27;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|||| | ||| ||| |||||
Db 7 CAGGGGACTCCATCACCATG 26

RESULT 5
AAZ66728/c
ID AAZ66728 standard; DNA; 47 BP.
XX
AC AAZ66728;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:1075.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 1; Page 460; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297

CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 15 A; 8 C; 14 G; 10 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 47;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CAGGTGTCTCGATCTCCATG 20
              ||| ||| || |||| ||||
Db         46 CAGATGTATCCATCTGCATG 27
```

RESULT 6
AAZ66820
ID AAZ66820 standard; DNA; 47 BP.
XX
AC AAZ66820;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:1167.
XX
KW *Human genome*; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 1; Page 479; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious *responses* to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX

SQ Sequence 47 BP; 10 A; 15 C; 8 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 47;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CAGGTGTCTCGATCTCCATG 20
              ||| ||| || |||| ||||
Db          2 CAGATGTATCCATCTGCATG 21
```

RESULT 7
AAX52340
ID AAX52340 standard; DNA; 50 BP.
XX
AC AAX52340;
XX
DT 25-JUN-1999 (first entry)
XX
DE Primer 28744.p (OLI555) used to isolate cDNA encoding PRO214.
XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW *congenital* microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
KW anti-thrombotic; wound healing; tissue repair; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9914328-A2.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US19330.
XX
PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.
PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059184.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.
PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 29-OCT-1997; 97US-0063735.

PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX
DR WPI; 1999-229533/19.
XX
PT New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration
XX
PS Example 17; Page 128; 320pp; English.
XX
CC Oligonucleotides AAX52276-532 represent PCR primers and probes used
CC to isolate and amplify cDNA encoding secreted and transmembrane human
CC proteins (see AAX52213-74 and AAY13344-403). The cDNA sequences are
CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
CC fetal brain, fetal liver and fetal retina. The encoded polypeptides
CC have specific uses based on their homology to known polypeptides,
CC e.g. PRO211 and PRO217 can be used for disorders associated with the
CC preservation and maintenance of gastrointestinal mucosa and the
CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
CC microvillus atrophy), skin diseases associated with abnormal
CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
CC lung squamous cell carcinoma of the vulva and gliomas), potent effects on
CC cell growth and development, diseases related to growth or survival of
CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,
CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for
CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor
CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia
CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287
CC polypeptides and portions may have therapeutic applications in wound
CC healing and tissue repair; PRO317 can be used for treating problems of
CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
CC in the heart of genital tract.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 20; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| |  |||
Db         24 CAAGTGTCTCGATGTGGATG 43
```

RESULT 8
AAX28444
ID AAX28444 standard; DNA; 50 BP.
XX
AC AAX28444;
XX
DT 22-JUN-1999 (first entry)
XX
DE EGF-like/FGF-8 homologue coding sequence primer SEQ ID No 62.
XX
KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue; primer;
KW FGF-8 homologue; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9914327-A2.
XX
PD 25-MAR-1999.
XX
PF 10-SEP-1998; 98WO-US18824.
XX
PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059114.
PR 17-SEP-1997; 97US-0059117.
PR 18-SEP-1997; 97US-0059263.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 24-OCT-1997; 97US-0062816.
PR 29-OCT-1997; 97US-0063704.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;
PI Roy M, Wood WI;
XX
DR WPI; 1999-229532/19.
XX
PT Antibodies against specific proteins overexpressed in tumours
XX
PS Example 1; Page 43; 130pp; English.
XX
CC This sequence represents a primer used to isolate DNA encoding a
CC protein recognised by the antibodies of the inveniton.
CC The invention relates to antibodies (Ab) that bind to any of the
CC polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;
CC PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit
CC expression and/or activity of (I) are used: (i) to inhibit growth of
CC tumours; and (ii) as diagnostic/prognostic reagents for detection or
CC quantification of (I) in cells or tissues, by standard immunoassays, with
CC overexpression being indicative of cancer. For therapeutic use, the Ab
CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.
CC Genes expressing (I), many of which are growth factor homologues, are
CC overexpressed in some cases of cancer.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 20; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| |  |||
Db         24 CAAGTGTCTCGATGTGGATG 43
```

RESULT 9
AAA77544
ID AAA77544 standard; DNA; 50 BP.
XX
AC AAA77544;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human PRO214 hybridisation probe SEQ ID NO:44.
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine; hybridisation; probe; PCR primer; ss.
XX
OS Homo sapiens.
XX

PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US28313.
XX
PR 01-DEC-1998; 98WO-US25108.
PR 16-DEC-1998; 98US-0112850.
PR 12-JAN-1999; 99US-0115554.
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
PI Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2000-412154/35.
XX
PT Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating diagnosing a cardiovascular, endothelial or
PT angiogenic disorders in mammals -
XX
PS Example 12; Page 122; 315pp; English.
XX
CC The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating diagnosing a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PRO expression such as cardiovascular, endothelial or
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|| |||||||||| | |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 10
AAA30035
ID AAA30035 standard; DNA; 50 BP.
XX
AC AAA30035;
XX
DT 09-AUG-2000 (first entry)
XX
DE Probe used in PRO214 nucleotide sequence identification.
XX
KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;
KW cell growth; proliferation; HT protein; fibrulin; ADEPT; probe;
KW antibody dependent enzyme mediated prodrug therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200015666-A2.
XX
PD 23-MAR-2000.
XX
PF 08-SEP-1999; 99WO-US20594.
XX
PR 10-SEP-1998; 98US-0099803.
PR 10-SEP-1998; 98WO-US18824.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;
XX
DR WPI; 2000-271386/23.
XX
PT New isolated antibodies which bind to specific polypeptides used for
PT diagnosis and treatment of neoplastic cell growth and proliferation -
XX
PS Example 3; Page 75; 200pp; English.
XX
CC This sequence represents a probe used in the identification of the
CC human PRO214 nucleotide sequence. PRO214 shares sequence homology with
CC the HT protein and fibrulin. The invention relates to isolated antibodies
CC which bind to a polypeptide. The "PRO" polypeptides are encoded by genes
CC which are over expressed in the genome of tumour cells. Vectors and host
CC cells comprising the nucleic acid encoding the antibodies are used in the
CC production of the antibodies. The antibodies and nucleic acids encoding
CC them are used for diagnosing a tumour in a mammal. The antibodies are
CC used for inhibiting the growth of tumour cells and identifying compounds
CC that inhibit a biological or immunological activity of and/or expression
CC of a PRO187, PRO533, PRO214, PRO240, PRO211, PRO230, PRO261, PRO246 or
CC PRO317 polypeptide. The antibody can be used in antibody dependent enzyme
CC mediated prodrug therapy (ADEPT) by conjugating the antibody to a
CC prodrug-activating enzyme which converts a prodrug to an anti-cancer
CC drug. The antibodies can be fluorescently labelled and monitored by light
CC microscopy, flow cytometry or fluorimetry for diagnosis and prognosis of
CC tumours.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|| |||||||||| | |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 11
AAF60355
ID AAF60355 standard; DNA; 50 BP.
XX
AC AAF60355;
XX
DT 27-APR-2001 (first entry)
XX
DE PRO214 probe #1.
XX
KW Cytostatic; PRO protein; tumour; cancer; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200105836-A1.

XX
PD 25-JAN-2001.
XX
PF 20-DEC-1999; 99WO-US30999.
XX
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28564.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
XX
DR WPI; 2001-091968/10.
XX
PT New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT useful for diagnosing and treating cancers -
XX
PS Example 3; Page 92; 196pp; English.
XX
CC The present invention relates to PRO proteins and coding sequences. The
CC present sequence is a probe for one such PRO coding sequence. It was
CC found that the PRO genes are amplified in the genome of tumour cells. The
CC gene amplification is expected to be associated with the overexpression
CC of the gene product and contributes to tumourigenesis. Therefore,
CC antagonists of PRO proteins are useful for the treatment of benign or
CC malignant tumours, leukaemias, lymphoid malignancies and other disorders
CC such as neuronal, glial, astrocytal, hypothalamic, glandular, epithelial,
CC inflammatory and immunologic disorders.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 22; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|| |||||||||| | |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 12
AAF72498
ID AAF72498 standard; DNA; 50 BP.
XX
AC AAF72498;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO polypeptide gene oligonucleotide OLI555.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation; PCR primer; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US04414.
XX
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 99WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-081051/09.
XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease) -
XX
PS Example 17; Page 166; 393pp; English.
XX
CC The present sequence is an oligonucleotide used in the isolation of one
CC of sixty one nucleic acids encoding novel secreted and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful for treating skin diseases
CC (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosum. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 22; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|| |||||||||| | |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 13
ABL01039
ID ABL01039 standard; DNA; 50 BP.
XX
AC ABL01039;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human SNP involving a gap oligonucleotide SEQ ID NO:1030.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein; ds.
XX
OS Homo sapiens.
XX

PN WO200138586-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US32311.
XX
PR 24-NOV-1999; 99US-0167383.
XX
PA (CURA-) CURAGEN CORP.
XX
PI *Shimkets RA, Leach M;*
XX
DR WPI; 2001-355949/37.
XX
PT Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
PT sequence polymorphism -
XX
PS Claim 1; Page 559; 674pp; English.
XX
CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC *oligonucleotides. The sequences from the present invention can have*
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the
CC polymorphic protein within appropriate physiological samples).
XX
SQ Sequence 50 BP; 9 A; 14 C; 17 G; 10 T; 0 other;

Query Match 68.0%; Score 13.6; DB 23; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
||||||||| || | | |||
Db 24 CAGGTGTCTTGAGCCCTATG 43

RESULT 14
ABK40295
ID ABK40295 standard; DNA; 50 BP.
XX
AC ABK40295;
XX
DT 15-JUL-2002 (first entry)
XX
DE Oligonucleotide probe for human PRO226 DNA.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW cytostatic; neuroprotective; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200153486-A1.
XX
PD 26-JUL-2001.
XX
PF 11-FEB-2000; 2000WO-US03565.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 05-JAN-2000; 2000WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/26.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX
PS Example 5; Page 110; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides (AAU86128-AAU86162) and the polynucleotide sequences
CC encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO
CC antibodies are useful for treating benign or malignant tumours
CC (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid
CC malignancies, other disorders such as neuronal, glial, astrocytal,
CC hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders,
CC inflammatory, immune and angiogenic disorders. The polynucleotide
CC sequences are also useful in gene therapy. The present sequence
CC represents a probe used in the methods of the present invention.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 24; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|| |||||||||| | |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 15
ACA54898
ID ACA54898 standard; DNA; 50 BP.
XX
AC ACA54898;
XX
DT 05-JUN-2003 (first entry)
XX
DE Secreted and transmembrane protein associated oligonucleotide #7.
XX
KW Human; secreted and transmembrane protein; gene therapy; psoriasis;
KW enterocolitis; gastrointestinal ulceration; skin disease;
KW keratinocyte differentiation; epithelial cancer; Alzheimer's disease;
KW squamous cell carcinoma; Parkinson's disease; inflammatory disease;
KW amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;
KW multiple sclerosis; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; wound repair; tissue re-growth; ss.
XX
OS *Homo sapiens.*

XX
PN US2003017463-A1.
XX
PD 23-JAN-2003.
XX
PF 11-JUL-2001; 2001US-0903640.
XX
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 01-DEC-1998; 98WO-US25108.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 11-FEB-2000; 2000WO-US03565.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 17-SEP-1997; 97US-059113P.
PR 17-SEP-1997; 97US-059115P.
PR 17-SEP-1997; 97US-059117P.
PR 17-SEP-1997; 97US-059119P.
PR 17-SEP-1997; 97US-059121P.
PR 17-SEP-1997; 97US-059122P.
PR 17-SEP-1997; 97US-059184P.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 15-OCT-1997; 97US-062125P.
PR 17-OCT-1997; 97US-062285P.
PR 17-OCT-1997; 97US-062287P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-062814P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063045P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 24-OCT-1997; 97US-063127P.
PR 24-OCT-1997; 97US-063128P.
PR 27-OCT-1997; 97US-063327P.
PR 27-OCT-1997; 97US-063329P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063542P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063549P.
PR 28-OCT-1997; 97US-063550P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063435P.
PR 29-OCT-1997; 97US-063704P.
PR 29-OCT-1997; 97US-063732P.
PR 29-OCT-1997; 97US-063734P.
PR 29-OCT-1997; 97US-063735P.
PR 29-OCT-1997; 97US-063738P.
PR 29-OCT-1997; 97US-064215P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 03-NOV-1997; 97US-064248P.
PR 07-NOV-1997; 97US-064809P.
PR 12-NOV-1997; 97US-065186P.
PR 17-NOV-1997; 97US-065846P.
PR 18-NOV-1997; 97US-065693P.
PR 21-NOV-1997; 97US-066120P.
PR 21-NOV-1997; 97US-066364P.
PR 24-NOV-1997; 97US-066453P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066511P.
PR 24-NOV-1997; 97US-066770P.
PR 24-NOV-1997; 97US-066772P.
PR 25-NOV-1997; 97US-066840P.
PR 12-DEC-1997; 97US-069425P.
PR 04-JUN-1998; 98US-088026P.
PR 10-SEP-1998; 98US-099803P.
PR 14-SEP-1998; 98US-100262P.
PR 17-SEP-1998; 98US-100858P.
PR 13-OCT-1998; 98US-104080P.
PR 20-NOV-1998; 98US-109304P.
PR 22-DEC-1998; 98US-113296P.
PR 07-JUL-1999; 99US-143048P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 18-SEP-2000; 2000US-0665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-341586/32.
XX
PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing
PT or treating inflammatory diseases, organ failure, atherosclerosis,
PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
PT Parkinson's disease -
XX
PS Example 17; Page 90; 473pp; English.
XX
CC The invention describes sixty one nucleic acids encoding PRO polypeptides
CC (secreted and transmembrane). The PRO polypeptides and nucleic acids are
CC useful in diagnosing or treating enterocolitis, gastrointestinal
CC ulceration, skin diseases associated with abnormal keratinocyte
CC differentiation, e.g. psoriasis or epithelial cancers such as squamous
CC cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic
CC lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,
CC asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, AIDS, cancer,
CC diabetic complications, or mutations in general. The polypeptides are
CC also useful for wound repair and associated therapies concerned with
CC re-growth of tissue. The PRO polypeptides and nucleic acid molecules
CC are also useful in gene therapy, and as molecular weight markers for
CC protein electrophoresis purposes. The anti-PRO antibodies may be used
CC in diagnostic assays for PRO, or for the affinity purification of PRO
CC from recombinant cell culture or natural sources. This sequence
CC represents a novel human PRO polypeptide associated oligonucleotide.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 25; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|| |||||||||| | |||
Db 24 CAAGTGTCTCGATGTGGATG 43

Search completed: January 28, 2004, 18:41:49

Job time : 156 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 18:38:32 ; Search time 1994 Seconds
(without alignments)
243.776 Million cell updates/sec

Title: US-09-920-671-80
Perfect score: 20
Sequence: 1 caggtgtctcgatctccatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 306466

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	14.2	71.0	71	28	BH810806	BH810806 SALK_0512
c	2	13.8	69.0	80	14	H55339	H55339 CHR220278 C
	3	13.6	68.0	23	28	AZ761953	AZ761953 1M0556K06
	4	13.2	66.0	58	13	BU491208	BU491208 604127974
	5	13	65.0	55	9	AA907571	AA907571 om09f08.s
	6	13	65.0	56	9	AA725701	AA725701 ai22b02.s
	7	13	65.0	56	9	AA905157	AA905157 ok06a04.s
c	8	12.6	63.0	48	28	AZ800696	AZ800696 2M0058B21
	9	12.6	63.0	54	29	CC029869	CC029869 3591_1_11
c	10	12.6	63.0	60	28	AZ425836	AZ425836 1M0206E15
c	11	12.6	63.0	61	9	AI182426	AI182426 uc24h10.r
	12	12.6	63.0	70	9	AA578307	AA578307 nl30e12.s
	13	12.6	63.0	71	28	AZ323688	AZ323688 1M0045F14
c	14	12.4	62.0	68	28	AZ537585	AZ537585 AST-2P881
	15	12.4	62.0	69	14	T12642	T12642 CHR90162 Ch
	16	12.2	61.0	60	29	CC249412	CC249412 XF002 Bay
	17	12.2	61.0	61	29	AL948303	AL948303 Arabidops
c	18	12.2	61.0	64	10	BF199394	BF199394 SWOv3MCAM
c	19	12.2	61.0	66	28	AZ827039	AZ827039 2M0103O11
	20	12.2	61.0	66	28	BH813871	BH813871 SALK_0654
c	21	12.2	61.0	67	9	AA623669	AA623669 vq72c10.s
	22	12.2	61.0	68	28	AZ537228	AZ537228 AST-2P030
c	23	12.2	61.0	73	9	AA658373	AA658373 nu22f07.s
	24	12.2	61.0	73	12	BJ051979	BJ051979 BJ051979
c	25	12.2	61.0	79	9	AA595959	AA595959 nn66d08.s
c	26	12.2	61.0	79	28	AQ025855	AQ025855 l(2)k0810
	27	12.2	61.0	80	10	BE449088	BE449088 ut52c07.y
	28	12	60.0	37	29	CC458682	CC458682 SALK_1216
c	29	12	60.0	39	12	BM280334	BM280334 3'EST-NCD
	30	12	60.0	45	28	BH023783	BH023783 BG02336-3
	31	12	60.0	50	9	AU103190	AU103190 AU103190
	32	12	60.0	50	9	AU104029	AU104029 AU104029
	33	12	60.0	50	9	AU105306	AU105306 AU105306
	34	12	60.0	59	9	AA082835	AA082835 zn21g12.s
c	35	12	60.0	63	28	AZ379841	AZ379841 1M0135H17
c	36	12	60.0	64	9	AA858284	AA858284 ob13a05.s
c	37	12	60.0	70	9	AI877307	AI877307 vz73e05.r
c	38	12	60.0	70	9	AA237942	AA237942 mx27e04.r
c	39	12	60.0	70	13	BU890908	BU890908 P043C09 P
c	40	12	60.0	70	14	N84707	N84707 J0579F Huma
c	41	12	60.0	74	13	BU815952	BU815952 N058C05 P
c	42	12	60.0	74	28	AZ615661	AZ615661 1M0445C02
	43	12	60.0	76	14	H96494	H96494 yt98g08.r1
	44	12	60.0	77	9	AV970179	AV970179 AV970179
c	45	12	60.0	78	14	H38724	H38724 yp62c08.r1

ALIGNMENTS

RESULT 1
BH810806/c
LOCUS BH810806 71 bp DNA linear GSS 02-MAY-2002
DEFINITION SALK_051224 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_051224, genomic survey sequence.
ACCESSION BH810806
VERSION BH810806.1 GI:20388624
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 71)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P. , Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

```
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES              Location/Qualifiers
     source           1. .71
                      /organism="Arabidopsis thaliana"
                      /mol_type="genomic DNA"
                      /strain="Columbia 0"
                      /db_xref="taxon:3702"
                      /clone="SALK_051224"
                      /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                      /note="PCR was performed on Arabidopsis thaliana lines
                      each of which contains  one or more TDNA insertion
                      elements. The resultant fragment for each  line was
                      directly sequenced to determine the genomic sequence at
                      the  site of insertion. Details of the protocols used can
                      be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       23 a     16 c     16 g     16 t
ORIGIN

  Query Match             71.0%;  Score 14.2;  DB 28;  Length 71;
  Best Local Similarity   84.2%;  Pred. No. 3e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCAT 19
              ||||| ||  |||||||||
Db         42 CAGGTTTCGTGATCTCCAT 24


RESULT 2
H55339/c
LOCUS       H55339                   80 bp    mRNA    linear   EST 07-DEC-1995
DEFINITION  CHR220278 Chromosome 22 exon Homo sapiens cDNA clone C22_346 5',
            mRNA sequence.
ACCESSION   H55339
VERSION     H55339.1  GI:1108205
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 80)
  AUTHORS   Trofatter,J.A., Long,K.R., Murrell,J.R., Stotler,C.J., Gusella,J.F.
            and Buckler,A.J.
  TITLE     An expression-independent catalog of genes from human chromosome 22
  JOURNAL   Genome Res. 5 (3), 214-224 (1995)
  MEDLINE   96159527
   PUBMED   8593609
COMMENT     Contact: Buckler AJ
            Molecular Neurogenetics Unit
            Massachusetts General Hospital
            Building 149, 13th St., Charlestown MA 02129
            Tel: 6177249616
            Fax: 6177265736
            Email: buckler@helix.mgh.harvard.edu
            Seq primer: T3.
FEATURES              Location/Qualifiers
     source           1. .80
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="C22_346"
                      /lab_host="E. coli DH5a"
                      /clone_lib="Chromosome 22 exon"
                      /note="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2:
                      Bam HI (destroyed); Exons were isolated from human
                      chromosome 22 specific cosmids  using a modification of
                      the method of exon amplification (Proc. Natl. Acad. Sci.
                      USA 88:4005-4009, 1991).   Amplified exons were digested
                      with Sal I and Bgl II and subsequently cloned into
                      pBluescriptIIKS+ at the Sal I and Bam HI sites."
BASE COUNT       32 a     15 c     23 g     10 t
ORIGIN

  Query Match             69.0%;  Score 13.8;  DB 14;  Length 80;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCC 17
              ||||||||| || ||||
Db         32 CAGGTGTCTTGAGCTCC 16


RESULT 3
AZ761953
LOCUS       AZ761953                 23 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0556K06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0556K06 R, genomic survey sequence.
ACCESSION   AZ761953
VERSION     AZ761953.1  GI:12871452
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0556  row: K  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0556K06"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        5 a      7 c      5 g      6 t
```

```
ORIGIN

  Query Match            68.0%;  Score 13.6;  DB 28;  Length 23;
  Best Local Similarity  80.0%;  Pred. No. 4.1e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              || ||| || |||||||| |
Db          1 CATGTGCCTTGATCTCCAGG 20


RESULT 4
BU491208
LOCUS       BU491208                 58 bp    mRNA    linear   EST 30-NOV-2002
DEFINITION  604127974F1 CSEQRBN37 Gallus gallus cDNA clone ChEST950c19 5', mRNA
            sequence.
ACCESSION   BU491208
VERSION     BU491208.1  GI:25984785
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology (UMIST
            )
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Layer and broiler"
                     /db_xref="taxon:9031"
                     /clone="ChEST950c19"
                     /sex="Male and female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="CSEQRBN37"
                     /note="Organ: pancreas; Vector: pBluescript II KS(+);
                     Site_1: EcoRI; Site_2: Not1; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with EcoRI
                     , size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
BASE COUNT       14 a     10 c     14 g     20 t
ORIGIN

  Query Match            66.0%;  Score 13.2;  DB 13;  Length 58;
  Best Local Similarity  83.3%;  Pred. No. 7.7e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCA 18
              ||||||| |  |||||||
Db         28 CAGGTGTGTACATCTCCA 45


RESULT 5
AA907571
LOCUS       AA907571                 55 bp    mRNA    linear   EST 10-JUN-1998
DEFINITION  om09f08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1540551 3' similar to gb:U02570 !!!! ALU CLASS C WARNING
            ENTRY !!!! (HUMAN);, mRNA sequence.
ACCESSION   AA907571
VERSION     AA907571.1  GI:3043031
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 1251  Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1540551"
                     /lab_host="DH10B"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
BASE COUNT       10 a     10 c     17 g     18 t
ORIGIN

  Query Match            65.0%;  Score 13;  DB 9;  Length 55;
  Best Local Similarity  100.0%;  Pred. No. 9.2e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGTCTCGATCTCC 17
              |||||||||||||
Db         41 TGTCTCGATCTCC 53


RESULT 6
AA725701
LOCUS       AA725701                 56 bp    mRNA    linear   EST 31-DEC-1998
DEFINITION  ai22b02.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343499 3'
            similar to gb:U02570 !!!! ALU CLASS C WARNING ENTRY !!!! (HUMAN);,
            mRNA sequence.
ACCESSION   AA725701
VERSION     AA725701.1  GI:2743408
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
            , Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 789   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .56
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="1343499"
                      /sex="male"
                      /lab_host="DH10B"
                      /clone_lib="Soares_testis_NHT"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was prepared from mRNA obtained from Clontech Laboratories
                      , Inc., and primed with  a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. 
                      Double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      went through one round of normalization to Cot5, and was
                      constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        9 a     10 c     17 g     20 t
ORIGIN

  Query Match             65.0%;  Score 13;  DB 9;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGTCTCGATCTCC 17
              |||||||||||||
Db         42 TGTCTCGATCTCC 54


RESULT 7
AA905157
LOCUS       AA905157                 56 bp    mRNA    linear   EST 09-JUN-1998
DEFINITION  ok06a04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1506990 3' similar to gb:U02570 !!!! ALU CLASS C WARNING
            ENTRY !!!! (HUMAN);, mRNA sequence.
ACCESSION   AA905157
VERSION     AA905157.1  GI:3040280
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 790   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .56
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1506990"
                      /lab_host="DH10B"
                      /clone_lib="Soares_NFL_T_GBC_S1"
                      /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      Equal amounts of plasmid DNA from three normalized
                      libraries (fetal lung NbHL19W, testis NHT, and B-cell
                      NCI_CGAP_GCB1) were mixed, and ss circles were made in
                      vitro. Following HAP purification, this DNA was used as
                      tracer in a subtractive hybridization reaction. The driver
                      was PCR-amplified cDNAs from pools of 5,000 clones made
                      from the same 3 libraries. The pools consisted of
                      I.M.A.G.E. clones 297480-302087, 682632-687239,
                      726408-728711, and 729096-731399. Subtraction by Bento
                      Soares and M. Fatima Bonaldo.  "
BASE COUNT       10 a     10 c     18 g     18 t
ORIGIN

  Query Match             65.0%;  Score 13;  DB 9;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGTCTCGATCTCC 17
              |||||||||||||
Db         42 TGTCTCGATCTCC 54


RESULT 8
AZ800696/c
LOCUS       AZ800696                 48 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0058B21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0058B21 R, genomic survey sequence.
ACCESSION   AZ800696
VERSION     AZ800696.1  GI:12953019
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0058  row: B  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 48.
FEATURES              Location/Qualifiers
     source           1. .48
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0058B21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 18 a 10 c 10 g 10 t
ORIGIN

Query Match 63.0%; Score 12.6; DB 28; Length 48;
Best Local Similarity 78.9%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCAT 19
||||| ||||| | ||||
Db 26 CAGGTATCTCGTTAGCCAT 8

RESULT 9
CC029869
LOCUS CC029869 54 bp DNA linear GSS 01-APR-2003
DEFINITION 3591_1_113_1_B12.2EL_x_1 3591 - RescueMu Grid P Zea mays genomic, genomic survey sequence.
ACCESSION CC029869
VERSION CC029869.1 GI:29444760
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 54)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3591_1_113_1 column: 9
Class: transposon-tagged.
FEATURES Location/Qualifiers
source 1. .54
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
BASE COUNT 10 a 14 c 25 g 5 t
ORIGIN

Query Match 63.0%; Score 12.6; DB 29; Length 54;
Best Local Similarity 78.9%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGTGTCTCGATCTCCATG 20
||||||| |||| ||| |
Db 33 AGGTGTCGCGATGCCCACG 51

RESULT 10
AZ425836/c
LOCUS AZ425836 60 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0206E15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0206E15 F, genomic survey sequence.
ACCESSION AZ425836
VERSION AZ425836.1 GI:10549945
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 60)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0206 row: E column: 15
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 60.
FEATURES Location/Qualifiers
source 1. .60
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0206E15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 25 a 11 c 11 g 13 t
ORIGIN

Query Match 63.0%; Score 12.6; DB 28; Length 60;
Best Local Similarity 78.9%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 AGGTGTCTCGATCTCCATG 20
              |||  | |||||||||| |
Db         20 ATGTTTCTCAATTTCCATG 2
```

RESULT 11
AI182426/c
LOCUS AI182426 61 bp mRNA linear EST 08-OCT-1998
DEFINITION uc24h10.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1398979 5' similar to TR:Q62433 Q62433 CYTOPLASMIC PROTEIN NDR1. ;, mRNA sequence.
ACCESSION AI182426
VERSION AI182426.1 GI:3733064
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 61)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:910695
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .61
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1398979"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NbMMG"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 13 a 15 c 19 g 14 t
ORIGIN

Query Match 63.0%; Score 12.6; DB 9; Length 61;
Best Local Similarity 78.9%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 AGGTGTCTCGATCTCCATG 20
              |||  | |||||||||| |
Db         52 AGGCCTTTCGATCTCCAGG 34
```

RESULT 12
AA578307
LOCUS AA578307 70 bp mRNA linear EST 12-SEP-1997
DEFINITION nl30e12.s1 NCI_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1042222 similar to SW:NULM_HUMAN P03901 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L ;, mRNA sequence.
ACCESSION AA578307
VERSION AA578307.1 GI:2356491
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 70)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Donald Orlic, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 282 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .70
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1042222"
/tissue_type="stem cells"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_HSC1"
/note="Organ: bone marrow; Vector: pAMP10; mRNA made from flow-sorted CD34+/CD38- hematopoietic stem cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing

Center"
BASE COUNT 17 a 21 c 17 g 15 t
ORIGIN

Query Match 63.0%; Score 12.6; DB 9; Length 70;
Best Local Similarity 78.9%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGTGTCTCGATCTCCATG 20
| | ||||| ||||||| |
Db 7 ACGAGTCTCAATCTCCAGG 25

RESULT 13
AZ323688
LOCUS AZ323688 71 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0045F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0045F14 F, genomic survey sequence.
ACCESSION AZ323688
VERSION AZ323688.1 GI:10378654
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 71)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: F column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 71.
FEATURES Location/Qualifiers
source 1. .71
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0045F14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 13 a 11 c 9 g 38 t
ORIGIN

Query Match 63.0%; Score 12.6; DB 28; Length 71;
Best Local Similarity 78.9%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGTGTCTCGATCTCCATG 20
| ||||||| | ||||||
Db 38 ATGTGTCTCATTTTCCATG 56

RESULT 14
AZ537585/c
LOCUS AZ537585 68 bp DNA linear GSS 06-NOV-2000
DEFINITION AST-2P881.ABI Genetrap PC-3 Human Prostatic Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.
ACCESSION AZ537585
VERSION AZ537585.1 GI:11114859
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 68)
AUTHORS Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M., Bernardino,A., Durick,K. and Pollok,B.
TITLE Exon-trap tags from a PC-3 GenomeScreen(TM) Library
JOURNAL Unpublished
COMMENT Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase proceeded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAmp-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.
Class: exon-trapped.
FEATURES Location/Qualifiers
source 1. .68
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Adenocarcinoma"
/cell_type="Epithelial"
/cell_line="PC-3"
/clone_lib="Genetrap PC-3 Human Prostatic Carcinoma Library"
/note="Organ: Prostate; Vector: pAmp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and used to transform DH5-alpha competent bacteria."
BASE COUNT 18 a 19 c 22 g 9 t
ORIGIN

Query Match 62.0%; Score 12.4; DB 28; Length 68;
Best Local Similarity 92.9%; Pred. No. 1.7e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGTGTCTCGATCTC 16
|||| |||||||||
Db 37 GGTGGCTCGATCTC 24

```
RESULT 15
T12642
LOCUS       T12642                    69 bp    mRNA    linear   EST 05-JAN-1994
DEFINITION  CHR90162 Chromosome 9 exon II Homo sapiens cDNA clone P94_116 5'
            and 3', mRNA sequence.
ACCESSION   T12642
VERSION     T12642.1  GI:439391
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 69)
  AUTHORS   Church,D.M., Stotler,C.J., Rutter,J.L., Murrell,J.R., Trofatter
            ,J.A. and Buckler,A.J.
  TITLE     Isolation of genes from complex sources of mammalian genomic DNA
            using exon amplification
  JOURNAL   Nat. Genet. 6, 98-105 (1994)
  MEDLINE   94184375
   PUBMED   8136842
COMMENT     Contact: Buckler AJ
            Molecular Neurogenetics Unit
            Massachusetts General Hospital
            Building 149, 13th St., Charlestown MA 02129
            Tel: 6177249616
            Fax: 6177265736
            Email: buckler@helix.mgh.harvard.edu
            Seq primer: T3 and T7.
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="P94_116"
                     /lab_host="E. coli DH5a"
                     /clone_lib="Chromosome 9 exon II"
                     /note="Vector: pBluescriptIIKS+; Exons were isolated from
                     human chromosome 9 specific cosmids  using a modification
                     of the method of exon amplification (Proc. Natl. Acad.
                     Sci. USA 88:4005-4009, 1991).   Amplified exons were
                     digested with SalI and BamHI and subsequently cloned into
                     pBluescriptIIKS+ at the SalI and BglII sites. "
BASE COUNT       15 a     21 c     18 g     15 t
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 14;  Length 69;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TCTCGATCTCCATG 20
              ||| ||||||||||
Db          3 TCTGGATCTCCATG 16


Search completed: January 28, 2004, 19:41:58
Job time : 2002 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 18:37:54 ; Search time 1494 Seconds
(without alignments)
547.652 Million cell updates/sec

Title: US-09-920-671-80
Perfect score: 20
Sequence: 1 caggtgtctcgatctccatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 1459972

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	13.8	69.0	57	9	AF084010	AF084010 Homo sapi
c	2	13.8	69.0	63	6	BD034085	BD034085 Sequence
c	3	13.6	68.0	47	6	AR289340	AR289340 Sequence
	4	13.6	68.0	47	6	AR289432	AR289432 Sequence
	5	13.6	68.0	50	6	AX076903	AX076903 Sequence
	6	13.6	68.0	50	6	AX165835	AX165835 Sequence
	7	13.6	68.0	50	6	AX201398	AX201398 Sequence
	8	13.6	68.0	50	6	AX697519	AX697519 Sequence
	9	13.6	68.0	50	6	BD075458	BD075458 Secretory
	10	13.6	68.0	50	6	BD172318	BD172318 Secreted
	11	13.6	68.0	50	6	BD172637	BD172637 Secreted
	12	13.6	68.0	50	6	BD172956	BD172956 Secreted
	13	13.6	68.0	50	6	BD173275	BD173275 Secreted
	14	13.6	68.0	50	6	BD175309	BD175309 Secretory
	15	13.6	68.0	61	6	AR118196	AR118196 Sequence
	16	13.6	68.0	61	6	BD130716	BD130716 High-affi
c	17	13.6	68.0	70	7	LAMDRL137	X70528 Bacteriopha
	18	13.4	67.0	26	6	AX486734	AX486734 Sequence
c	19	13.4	67.0	51	6	AX162361	AX162361 Sequence
c	20	13.2	66.0	39	6	AR013977	AR013977 Sequence
c	21	13.2	66.0	50	6	AX589636	AX589636 Sequence
	22	13.2	66.0	60	6	AR118191	AR118191 Sequence
	23	13.2	66.0	60	6	BD130711	BD130711 High-affi
	24	13.2	66.0	64	6	AR013979	AR013979 Sequence
c	25	13.2	66.0	66	6	AR013976	AR013976 Sequence
	26	13	65.0	66	6	AR173253	AR173253 Sequence
	27	13	65.0	66	6	BD087206	BD087206 Mammalian
c	28	12.8	64.0	40	6	AX260247	AX260247 Sequence
	29	12.8	64.0	47	6	AR291001	AR291001 Sequence
c	30	12.8	64.0	47	6	AR291230	AR291230 Sequence
	31	12.8	64.0	50	6	AX613046	AX613046 Sequence
c	32	12.8	64.0	60	6	AX601350	AX601350 Sequence
c	33	12.8	64.0	60	6	BD180765	BD180765 Array of
	34	12.6	63.0	20	6	AR200655	AR200655 Sequence
	35	12.6	63.0	21	6	AR067340	AR067340 Sequence
c	36	12.6	63.0	24	6	AX743920	AX743920 Sequence
c	37	12.6	63.0	25	6	AX613481	AX613481 Sequence
	38	12.6	63.0	26	6	I28831	I28831 Sequence 67
c	39	12.6	63.0	27	6	AR150679	AR150679 Sequence
c	40	12.6	63.0	27	6	E16228	E16228 Primer. 7/1
c	41	12.6	63.0	27	6	E27240	E27240 Novel physi
c	42	12.6	63.0	27	6	E28312	E28312 Utilization
c	43	12.6	63.0	36	6	AX008695	AX008695 Sequence
	44	12.6	63.0	38	6	E52280	E52280 Ligated glu
	45	12.6	63.0	62	6	AX427184	AX427184 Sequence

ALIGNMENTS

RESULT 1
AF084010/c
LOCUS AF084010 57 bp mRNA linear PRI 17-MAY-1999
DEFINITION Homo sapiens T cell receptor beta chain (TCRB) mRNA, partial cds.
ACCESSION AF084010
VERSION AF084010.1 GI:4836183
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 57)
AUTHORS Pachman,L.M., Liotta,M.R., Caliendo,J., Greene,M., Pope,R.M.,
Morrello,F., Lawton,T., Crawford,S., Wu,T.T. and O'Gorman,M.R.G.
TITLE New Onset Juvenile Dermatomyositis: Muscle Biopsy

```
            Immunohistochemistry and T-Cell Receptor Studies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 57)
  AUTHORS   Pachman,L.M., Liotta,M.R., Lawton,T. and Wu,T.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-AUG-1998) Pediatric Immunology, CMIER/Children's
            Memorial Medical Center, 2300 Children's Plaza Box #50, Chicago, IL
            60614, USA
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="7"
                     /map="7q35-q36"
                     /note="from new onset juvenile dermatomyositis patient"
     gene            <1. .>57
                     /gene="TCRB"
     CDS             <1. .>57
                     /gene="TCRB"
                     /note="T cell receptor beta chain 5.1; V beta 8, J beta
                     2.5"
                     /codon_start=1
                     /product="T cell receptor beta chain"
                     /protein_id="AAD30372.1"
                     /db_xref="GI:4836184"
                     /translation="VYFCASRPREIETQYFGPG"
BASE COUNT       12 a     17 c     18 g     10 t
ORIGIN

  Query Match             69.0%;  Score 13.8;  DB 9;  Length 57;
  Best Local Similarity   88.2%;  Pred. No. 1.9e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GTGTCTCGATCTCCATG 20
              | ||||||||||||  ||
Db         40 GGGTCTCGATCTCCCTG 24


RESULT 2
BD034085/c
LOCUS       BD034085                  63 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sequence tag and encoded human protein.
ACCESSION   BD034085
VERSION     BD034085.1  GI:22575827
KEYWORDS    JP 2001269182-A/10331.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
  TITLE     Sequence tag and encoded human protein
  JOURNAL   Patent: JP 2001269182-A 10331 02-OCT-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001269182-A/10331
            PD   02-OCT-2001
            PF   24-FEB-2000 JP 2000118773
            PR   26-FEB-1999 US    60/122487
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
            PI   JORDAN
            PC   C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
              G06F15/40
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT       14 a     14 c     25 g      9 t      1 others
ORIGIN

  Query Match             69.0%;  Score 13.8;  DB 6;  Length 63;
  Best Local Similarity   88.2%;  Pred. No. 1.9e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGTGTCTCGATCTCCAT 19
              ||||||| | |||||||
Db         57 GGTGTCTGGGTCTCCAT 41


RESULT 3
AR289340/c
LOCUS       AR289340                  47 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1075 from patent US 6537751.
ACCESSION   AR289340
VERSION     AR289340.1  GI:31676624
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 1075 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       14 a      8 c     14 g     10 t      1 others
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              ||| ||| || |||| ||||
Db         46 CAGATGTATCCATCTGCATG 27


RESULT 4
AR289432
LOCUS       AR289432                  47 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1167 from patent US 6537751.
ACCESSION   AR289432
VERSION     AR289432.1  GI:31676716
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 1167 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       10 a     14 c      8 g     14 t      1 others
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              ||| ||| || |||| ||||
Db          2 CAGATGTATCCATCTGCATG 21


RESULT 5
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```
AX076903
LOCUS       AX076903                50 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 15 from Patent WO0105836.
ACCESSION   AX076903
VERSION     AX076903.1  GI:13121562
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and
            Wood,W.I.
  TITLE     Polypeptidic compositions and methods for the treatment of tumors
  JOURNAL   Patent: WO 0105836-A 15 25-JAN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide Probe"
BASE COUNT        9 a     10 c     18 g     13 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| |  |||
Db         24 CAAGTGTCTCGATGTGGATG 43


RESULT 6
AX165835
LOCUS       AX165835                50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1030 from Patent WO0138586.
ACCESSION   AX165835
VERSION     AX165835.1  GI:14546664
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0138586-A 1030 31-MAY-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg43986426"
     variation       26
                     /note="single nucleotide polymorphism"
BASE COUNT        9 a     14 c     17 g     10 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              |||||||||  || | | |||
Db         24 CAGGTGTCTTGAGCCCTATG 43


RESULT 7
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```
AX201398
LOCUS       AX201398                50 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 77 from Patent WO0153486.
ACCESSION   AX201398
VERSION     AX201398.1  GI:15391199
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
            Stone,D.M., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of tumour
  JOURNAL   Patent: WO 0153486-A 77 26-JUL-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide Probe."
BASE COUNT        9 a     10 c     18 g     13 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| |  |||
Db         24 CAAGTGTCTCGATGTGGATG 43


RESULT 8
AX697519
LOCUS       AX697519                50 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 110 from Patent WO0104311.
ACCESSION   AX697519
VERSION     AX697519.1  GI:29498631
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N.,
            Filvaroff,E., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
            Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J.,
            Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
            Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0104311-A 110 18-JAN-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide Probe"
BASE COUNT        9 a     10 c     18 g     13 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| |  |||
Db         24 CAAGTGTCTCGATGTGGATG 43


RESULT 9
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```
BD075458
LOCUS       BD075458                 50 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Secretory and transmembrane polypeptide and nucleic acid encoding
            the same.
ACCESSION   BD075458
VERSION     BD075458.1  GI:22621061
KEYWORDS    JP 2001516580-A/91.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
  TITLE     Secretory and transmembrane polypeptide and nucleic acid encoding
            the same
  JOURNAL   Patent: JP 2001516580-A 91 02-OCT-2001;
            GENENTECH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001516580-A/91
            PD   02-OCT-2001
            PF   16-SEP-1998 JP 2000511867
            PR   17-SEP-1997 US    60/059115,17-SEP-1997 US    60/059184 PR
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            25-NOV-1997 US    60/066840
            PI   WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI
              JEAN CHEN,
            PI   JEAN YUAN
            PC   C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,
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            PC   C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02//(C12P21/08, PC
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ORIGIN

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Qy          1 CAGGTGTCTCGATCTCCATG 20
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Db         24 CAAGTGTCTCGATGTGGATG 43
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LOCUS       BD172318                 50 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Secreted and transmembrane polypeptides and nucleic acids encoding
            the same.
ACCESSION   BD172318
VERSION     BD172318.1  GI:28413618
KEYWORDS    JP 2002223786-A/91.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
            Yuan,J.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: JP 2002223786-A 91 13-AUG-2002;
            GENENTECH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002223786-A/91
            PD   13-AUG-2002
            PF   18-DEC-2001 JP 2001385135
            PR   17-SEP-1997 US    60/059115,17-SEP-1997 US    60/059184 PR
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            24-NOV-1997 US    60/066453,25-NOV-1997 US    60/066840 PI
            WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
            JIAN ZHENG,
            PI   JEAN YUAN
            PC   C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
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ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
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Db         24 CAAGTGTCTCGATGTGGATG 43


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LOCUS       BD172637                  50 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Secreted and transmembrane polypeptides and nucleic acids encoding
            the same.
ACCESSION   BD172637
VERSION     BD172637.1  GI:28413939
KEYWORDS    JP 2002238586-A/91.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
            Yuan,J.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: JP 2002238586-A 91 27-AUG-2002;
            GENENTECH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002238586-A/91
            PD   27-AUG-2002
            PF   18-DEC-2001 JP 2001385205
            PR   17-SEP-1997 US    60/059115,17-SEP-1997 US    60/059184 PR
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            17-NOV-1997 US    60/065846,18-NOV-1997 US    60/065693 PR
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            WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
            JIAN ZHENG,
            PI   JEAN YUAN
            PC   C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),
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  Query Match           68.0%;  Score 13.6;  DB 6;  Length 50;
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  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
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Db         24 CAAGTGTCTCGATGTGGATG 43


RESULT 12
BD172956
LOCUS       BD172956                  50 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Secreted and transmembrane polypeptides and nucleic acids encoding
            the same.
ACCESSION   BD172956
VERSION     BD172956.1  GI:28414262
KEYWORDS    JP 2002238587-A/91.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
            Yuan,J.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: JP 2002238587-A 91 27-AUG-2002;
            GENENTECH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002238587-A/91
            PD   27-AUG-2002
            PF   18-DEC-2001 JP 2001385248
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            JIAN ZHENG,
            PI   JEAN YUAN
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  Query Match             68.0%;  Score 13.6;  DB 6;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
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Db         24 CAAGTGTCTCGATGTGGATG 43


RESULT 13
BD173275
LOCUS       BD173275                  50 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Secreted and transmembrane polypeptides and nucleic acids encoding
            the same.
ACCESSION   BD173275
VERSION     BD173275.1  GI:28414586
KEYWORDS    JP 2002238588-A/91.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
            Yuan,J.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: JP 2002238588-A 91 27-AUG-2002;
            GENENTECH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002238588-A/91
            PD   27-AUG-2002
            PF   18-DEC-2001 JP 2001385315
            PR   17-SEP-1997 US    60/059115,17-SEP-1997 US    60/059184 PR
            17-SEP-1997 US    60/059122,17-SEP-1997 US    60/059117 PR
            17-SEP-1997 US    60/059113,17-SEP-1997 US    60/059121 PR
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            JIAN ZHENG,
            PI   JEAN YUAN
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ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CAGGTGTCTCGATCTCCATG 20
              || |||||||||| |  |||
Db         24 CAAGTGTCTCGATGTGGATG 43


RESULT 14
BD175309
LOCUS       BD175309                  50 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Secretory and transmembrane polypeptide and nucleic acid encoding
            the same.
ACCESSION   BD175309
VERSION     BD175309.1  GI:29121005
KEYWORDS    JP 2002253280-A/91.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
            Yuan,J.
  TITLE     Secretory and transmembrane polypeptide and nucleic acid encoding
            the same
  JOURNAL   Patent: JP 2002253280-A 91 10-SEP-2002;
            GENENTECH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002253280-A/91
            PD   10-SEP-2002
            PF   18-DEC-2001 JP 2001385319
            PR   17-SEP-1997 US    60/059115,17-SEP-1997 US    60/059184 PR
            17-SEP-1997 US    60/059122,17-SEP-1997 US    60/059117 PR
            17-SEP-1997 US    60/059113,17-SEP-1997 US    60/059121 PR
            17-SEP-1997 US    60/059119,18-SEP-1997 US    60/059263 PR
            18-SEP-1997 US    60/059266,15-OCT-1997 US    60/062125 PR
            17-OCT-1997 US    60/062287,17-OCT-1997 US    60/062285 PR
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            24-NOV-1997 US    60/066453,25-NOV-1997 US    60/066840 PI
            WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
            JIAN ZHENG,
            PI   JEAN YUAN
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REFERENCE   1  (bases 1 to 61)
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